Supplementary Table 1: Bulk RNA-seq vs. single cell RNA-seq

Bulk RNA-seq	Single Cell RNA-seq
Number of reads is limiting	Tiny amount of starting RNA is limiting
Some coverage bias due to random hexamer priming	Strong 3’ bias due to poly(A) priming
Not as much amplification needed	Large amount of amplification introduces noise
Generally small number of replicates	Usually want at least 80-90 cells (low coverage)
N-group design (tumor vs. normal, time course, etc.)	Often single group design
Highly sensitive; can detect transcripts present at very low concentrations	Low capture efficiency means that rare transcripts are often missed